

OM nucleic - nucleic search, using sw model

Run on: August 17, 2005, 18:01:27 ; Search time 3856 Seconds
(without alignments)
10429.935 Million cell updates/sec

Title: US-10-021-753A-1
Perfect score: 830
Sequence: 1 ccccccgagcgcgcgcgcg.....catttaactcatttgagag 830

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 20

Total number of hits satisfying chosen parameters: 691

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_un.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Score Match	Query Length	DB ID	Description
1	830 100.0	830 6	BD186306	BD186306 STAT6 act
2	830 100.0	830 6	AX337063	AX337063 Sequence
3	830 100.0	830 9	HSTUMP	X16064 Human mRNA
4	829 99.9	830 6	AX590153	AX590153 Sequence
5	829 99.9	831 6	CQ725369	CQ725369 Sequence
6	821 98.9	840 9	BC003352	BC003352 Homo sapi
7	821 98.9	858 9	BC052333	BC052333 Homo sapi
8	820 98.8	841 9	AK130847	AK130847 Homo sapi
9	814 98.1	865 9	AY117678	AY117678 Homo sapi
10	700 84.3	818 9	BC012431	BC012431 Homo sapi
11	645 77.7	645 6	CQ832420	CQ832420 Sequence
12	634 76.4	1134 9	BC022436	BC022436 Homo sapi

13	609 73.4	938 6	AX405763	AX405763 Sequence
14	577 69.5	599 6	AX381150	AX381150 Sequence
15	563 67.8	563 9	HUMCH13C4A	L13806 Homo sapien
16	539 64.9	539 6	CQ671453	CQ671453 Sequence
17	519 62.5	519 6	AX806477	AX806477 Sequence
c 18	519 62.5	519 6	AX956373	AX956373 Sequence
19	519 62.5	519 9	CR457036	CR457036 Homo sapi
20	519 62.5	577 6	AX381508	AX381508 Sequence
21	516 62.2	516 6	BD142401	BD142401 An insuli
22	512 61.7	819 9	HSMF21HOM	X64899 H.sapiens m
23	501 60.4	519 9	AY334563	AY334563 Homo sapi
24	496 59.8	506 6	AX393798	AX393798 Sequence
c 25	480 57.8	531 6	AX396789	AX396789 Sequence
26	475 57.2	499 6	CQ713515	CQ713515 Sequence
27	474 57.1	535 6	AX396495	AX396495 Sequence
28	465 56.0	465 6	CQ691284	CQ691284 Sequence
29	465 56.0	465 6	CQ693052	CQ693052 Sequence
30	457 55.1	471 6	AX340927	AX340927 Sequence
31	456 54.9	467 6	AX339997	AX339997 Sequence
32	453 54.6	465 6	CQ699300	CQ699300 Sequence
33	445 53.6	447 6	CQ679650	CQ679650 Sequence
34	440 53.0	469 6	CQ696611	CQ696611 Sequence
35	439 52.9	890 6	AX283790	AX283790 Sequence
36	433 52.2	467 6	CQ713036	CQ713036 Sequence
37	431 51.9	472 6	CQ683000	CQ683000 Sequence
38	429 51.7	632 6	AX198580	AX198580 Sequence
39	429 51.7	632 6	AX209119	AX209119 Sequence
40	425 51.2	433 6	AX393787	AX393787 Sequence
41	424 51.1	424 6	CQ663748	CQ663748 Sequence
c 42	420 50.6	420 6	AX397225	AX397225 Sequence
43	420 50.6	670 6	CQ693950	CQ693950 Sequence
44	411 49.5	513 6	AX393690	AX393690 Sequence
45	409 49.3	522 6	AX396097	AX396097 Sequence

ALIGNMENTS

RESULT 1
BD186306 LOCUS BD186306 830 bp DNA linear PAT 17-JUN-2003
DEFINITION STAT6 activating gene.
ACCESSION BD186306
VERSION BD186306.1 GI:31878606
KEYWORDS WO 02096943-A/175.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 830)
AUTHORS Honda,G., Matsuda,A., Muramatsu,S. and Ishizawa,K.
TITLE STAT6 activating gene
JOURNAL Patent: WO 02096943-A 175 05-DEC-2002;
ASAHI KASEI CORP,GOICHI HONDA,AKIO MATSUDA,SHUJI MURAMATSU, KENYA ISHIZAWA
COMMENT OS Homo sapiens (human)
PN WO 02096943-A/175
PD 05-DEC-2002
PF 22-MAY-2002 WO 2002JP004949
PR 25-MAY-2001 JP 01P 157043.30-AUG-2001 JP 01P 260681 PR
10-OCT-2001 JP 01P 313175
PI GOICHI HONDA,AKIO MATSUDA,SHUJI MURAMATSU,KENYA ISHIZAWA PC
C07K14/47,C07K17/00,C12N15/12,C12N5/10,C12P21/02,C12P21/08, PC
C12Q1/02.
PC A61P3/06,A61P3/10,A61P29/00,A61P31/00,A61P35/00,A61P37/00, PC
G01N33/15.

Search completed: August 18, 2005, 07:43:29
Job time : 3866 secs

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2005, 17:41:12 ; Search time 559 Seconds
(without alignments)
8789.598 Million cell updates/sec

Title: US-10-021-753A-1
Perfect score: 830
Sequence: 1 ccccccgagcgccgcgcg.....catttaactcatttgagag 830

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 20

Total number of hits satisfying chosen parameters: 274

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Database : N_Geneseqn_16Dec04:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	%		
No.	Score	Match	Length	DB ID
Description				
1	830	100.0	830	6 ABL69235
2	830	100.0	830	6 ABK84540
3	830	100.0	830	6 ABK84540 Human cDN
4	830	100.0	830	6 ABK86326
5	830	100.0	830	8 ABX10438
6	830	100.0	830	10 ADG10759
7	830	100.0	838	2 ACN39630
8	829	99.9	830	8 ABX6594
9	821	98.9	852	10 ADG32861
10	821	98.9	1235	10 ADE08897
11	810	97.6	810	10 ADF85755

12	760	91.6	834	10 ACC79008	Ac79008 Human TCP
13	645	77.7	645	12 ADQ92103	Adq92103 Human aut
c 14	622	74.9	823	12 ADP02981	Adp02981 Human hou
c 15	622	74.9	823	13 ADS88479	Ads88479 Human hou
16	609	73.4	938	6 ABN59767	Abn59767 Human hou
17	596	71.8	951	2 AAQ05238	Aaq05238 Sequence
18	590	71.1	590	6 ABV88032	Abv88032 Human col
19	579	69.8	616	8 ABZ20317	Abz20317 Group III
20	577	69.5	599	6 ABK54618	Abk54618 Human col
21	570	68.7	687	5 AAS90222	Aas90222 DNA encod
22	543	65.4	976	10 ADE07129	Ade07129 Novel cod
23	532	64.1	532	6 ABV87963	Abv87963 Human col
24	519	62.5	519	10 ADD26670	Add26670 Human adi
c 25	519	62.5	519	12 ADE65884	Ade65884 Antisense
26	519	62.5	577	6 ABK54976	Abk54976 Human tum
27	516	62.2	516	6 ABK49328	Abk49328 Human tum
28	496	59.8	506	6 ABK53992	Abk53992 Human hea
c 29	480	57.8	531	6 ABK45453	Abk45453 cDNA enco
30	474	57.1	535	6 ABK45159	Abk45159 cDNA enco
31	470	56.6	521	6 ABV87714	Abv87714 Human col
32	465	56.0	703	6 ABQ60526	Abq60526 Human col
33	461	55.5	490	6 ABV87148	Abv87148 Human col
34	458	55.2	508	9 ACH34099	Ach34099 Human end
35	457	55.1	471	6 ABL37585	Ab137585 Human col
36	456	54.9	467	6 ABL36655	Ab136655 Human col
37	452	54.5	502	9 ACH33708	Ach33708 Human end
38	441	53.1	490	9 ACH24859	Ach24859 Human adu
39	439	52.9	490	6 ABV87288	Abv87288 Human col
40	439	52.9	890	6 AAS61936	Aas61936 Porcine m
41	438	52.8	466	9 ACH35114	Ach35114 Human end
42	429	51.7	632	4 AAS24778	Aas24778 Human ova
43	429	51.7	632	5 AAH83411	Aah83411 Human ova
44	425	51.2	433	6 ABK53981	Abk53981 Human bea
45	422	50.8	423	9 ACH18358	Ach18358 Human adu

ALIGNMENTS

RESULT 1	
ABL69235	
ID ABL69235 standard: DNA: 830 BP.	
XX	
AC ABL69235:	
XX	
DT 15-MAY-2002 (first entry)	
XX	
DE Prostate cancer related gene sequence SEQ ID NO:7572.	
XX	
KW Human: cancer: colon: breast: ovary: oesophagus: kidney: thyroid:	
KW stomach: lung: prostate: pancreas: carcinoma: antitumour: cancerous:	
KW cytosolic: gene therapy: antineoplastic: Wilms' tumour: adenocarcinoma:	
KW gene: ds.	
XX	
OS Homo sapiens.	
XX	
PN WO200194629-A2.	
XX	
PD 13-DEC-2001.	
XX	
PF 30-MAY-2001: 2001WO-US010838.	
XX	
PR 05-JUN-2000: 2000US-0209473P.	
PR 05-JUN-2000: 2000US-0209531P.	
PR 18-SEP-2000: 2000US-0233133P.	
PR 18-SEP-2000: 2000US-0233617P.	